WEST Search History

DATE: Saturday, March 09, 2002

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,PGPB; PLUR=YES; OP=ADJ		
L15	ferment$7 and l11	1520	L15
L14	L13 and l8	0	L14
L13	phosphoribosyl pyrophosphate synthetase and l11	1	L13
L12	phosphoribosyl pyrophosphate amidotransferase and l11	0	L12
L11	l10 and l9	8642	L11
L10	purine$1 or ADENOSINE or GUANOSINE or INOSINE or XANTHOSINE or Purine ribonucleoside	22578	L10
L9	Escherichia coli or e coli or Paracolobactrum coliforme	39832	L9
L8	l7 or l6 or l5 or l4 or l3 or l2 or l1	3848	L8
L7	(((435/252.8)!.CCLS.))	203	L7
L6	(((435/243)!.CCLS.))	914	L6
L5	(((435/194)!.CCLS.))	801	L5
L4	(((435/193)!.CCLS.))	805	L4
L3	(((435/183)!.CCLS.))	1225	L3
L2	(((435/88)!.CCLS.))	120	L2
L1	((435/87)!.CCLS.)	87	L1

END OF SEARCH HISTORY

WEST

End of Result Set

Generate Collection | Print

L13: Entry 1 of 1 File: USPT Jan 1, 2002

US-PAT-NO: 6335170
DOCUMENT-IDENTIFIER: US 6335170 B1

TITLE: Gene expression in bladder tumors

DATE-ISSUED: January 1, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Orntoft; Torben F.	DK 8230 Aabyhoj			DKX

APPL-NO: 9/ 510643 [PALM]
DATE FILED: February 22, 2000

PARENT-CASE:
This application claims the benefit of U.S. Provisional Application No. 60/121,124, filed Feb. 22, 1999, which is hereby incorporated by reference in its entirety.

INT-CL: [7] C12 Q 1/68, C12 P 19/34, C07 H 21/02

US-CL-ISSUED: 435/6; 435/91.1, 435/91.2, 536/23.1, 536/24.3, 536/24.31, 536/24.33
US-CL-CURRENT: 435/6; 435/91.1, 435/91.2, 536/23.1, 536/24.3, 536/24.31, 536/24.33

FIELD-OF-SEARCH: 435/6, 435/91.1, 435/91.2, 536/23.1, 536/24.3, 536/24.31, 536/24.33

PRIOR-ART-DISCLOSED:

U.S. PATENT DOCUMENTS

Search Selected | Search ALL

	PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
☐	5677125	October 1997	Holt et al.	435/6
☐	5700637	December 1997	Southern	435/6

FOREIGN PATENT DOCUMENTS

FOREIGN-PAT-NO	PUBN-DATE	COUNTRY	US-CL
198 18 619	October 1999	DEX	
89/10977	November 1989	WOX	
96/30389	October 1996	WOX	
97/16206	May 1997	WOX	
97/28446	August 1997	WOX	
98/53319	November 1998	WOX	
99/47674	September 1999	WOX	

OTHER PUBLICATIONS

Liebert et al, "Identification of new biomarkers for bladder cancer using the differential display reverse transcriptase polymerase chain reaction", Proc. Am. Assn. Cancer Res. 38:287, Abstract 1928, Mar. 1997.*
Liebert et al, "Novel molecular markers fof bladder cancer revealed by differential display reverse transcriptase polymerase chain reaction", J. Urol. 159(5 suppl.) 286, Abstract 1101, May 1998.*
Peter S. Nelson, et al., "An Expressed-Sequence-Tag Database of the Human Prostate: Sequence Analysis of 1168 cDNA Clones", Genomics 47, pp. 12-25, 1998.
David B. Krizman, et al., "Construction of a Representative cDNA Library from Prostatic Intraepithelial Neoplasia", Cancer Research 56, pp. 5380-5383, Dec. 1, 1996.
Victoria Hawkins, et al., "PEDB: The Prostate Expression Database", Nucleic Acids Research, vol. 27,No. 1, pp. 240-208, 1999.
Lin Zhang, et al., "Gene Expression Profiles in Normal and Cancer Cells", Science, vol. 276,pp. 1268-1272, May 23, 1997.
Torben F. Orntoft, et al., "Molecular Alterations in Bladder Cancer", United Editorial, XP-000971351, Nov. 11, 1997.
Margaret A. Knowles, et al., Molecular Genetics of Bladder Cancer: Pathways of Development and Progression, Cancer Surveys, vol. 31, pp. 49-76, 1998.

ART-UNIT: 1655
PRIMARY-EXAMINER: Fredman; Jeffrey
ATTY-AGENT-FIRM: Banner & Witcoff, Ltd.

ABSTRACT:

Methods for analyzing tumor cells, particularly bladder tumor cells employ gene expression analysis of samples. Gene expression patterns are formed and compared to reference patterns. Alternatively gene expression patterns are manipulated to exclude genes which are expressed in contaminating cell populations. Another alternative employs subtraction of the expression of genes which are expressed in contaminating cell types. These methods provide improved accuracy as well as alternative basis for analysis from diagnostic and prognostic tools currently available.

21 Claims, 24 Drawing figures

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=> d full his

     (FILE 'HOME' ENTERED AT 13:16:37 ON 09 MAR 2002)

     FILE 'REGISTRY' ENTERED AT 13:22:52 ON 09 MAR 2002
L1             1 SEA ABB=ON  PLU=ON  PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE/CN

               D

     FILE 'HCAPLUS' ENTERED AT 13:23:21 ON 09 MAR 2002

     FILE 'REGISTRY' ENTERED AT 13:23:25 ON 09 MAR 2002
               SET SMARTSELECT ON
L2             SEL PLU=ON  L1 1- CHEM :      16 TERMS
               SET SMARTSELECT OFF

     FILE 'HCAPLUS' ENTERED AT 13:23:25 ON 09 MAR 2002
L3           514 SEA ABB=ON  PLU=ON  L2
L4        209873 SEA ABB=ON  PLU=ON  ESCHERICHIA COLI OR E# COLI OR PARACOLOBACT
               RUM COLIFORME
L5          6105 SEA ABB=ON  PLU=ON  PURINE NUCLEOSIDE# OR (NUCLEOSIDES (L)
               PURINE) OR PURINE RIBONUCLEOSIDE#
L6             2 SEA ABB=ON  PLU=ON  L3 (L) L4 (L) L5
               D IBIB AB 1-2
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=> d ibib ab 1-2

L6 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:77676 HCAPLUS
DOCUMENT NUMBER: 130:152661
TITLE: Escherichia containing mutants of enzymes associated with improved biosynthesis of purine nucleosides by fermentation
INVENTOR(S): Matsui, Hiroshi; Kawasaki, Hisashi; Shimaoka, Megumi; Takenaka, Yasuhiro; Kurahashi, Osamu
PATENT ASSIGNEE(S): Ajinomoto Co., Inc., Japan
SOURCE: PCT Int. Appl., 72 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9903988	A1	19990128	WO 1998-JP3239	19980717
W: BR, CN, ID, JP, KR, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 1004663	A1	20000531	EP 1998-932584	19980717
R: DE, FR, GB, IT				
BR 9815557	A	20010717	BR 1998-15557	19980717

PRIORITY APPLN. INFO.: JP 1997-194603 A 19970718
WO 1998-JP3239 W 19980717

AB An Escherichia strain capable of producing **purine nucleosides** with improved yield is characterized as having (1) a PRPP (phosphoribosyl pyrophosphate) amidotransferase (encoded by gene purF) or **PRPP synthase** (gene prs) mutant lacking feedback inhibition; (2) inactivated **purine** repressor; (3) blocked synthetic pathway catalyzed by, e.g., succinyl-adenosine monophosphate synthase, that leads to the synthesis of other metabolic products; and/or (4) reduced ability of the nucleoside permease-regulated cellular up-taking of **purine nucleosides**. Prepn. of mutants from **Escherichia coli** K12 strain W3110 was demonstrated.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1982:540764 HCAPLUS
DOCUMENT NUMBER: 97:140764
TITLE: Phosphoribosyl pyrophosphate synthetase of Escherichia coli. Identification of a mutant enzyme
AUTHOR(S): Hove-Jensen, Bjarne; Nygaard, Per
CORPORATE SOURCE: Inst. Biol. Chem. B, Univ. Copenhagen, Copenhagen, Den.
SOURCE: Eur. J. Biochem. (1982), 126(2), 327-32
CODEN: EJBCAI; ISSN: 0014-2956
DOCUMENT TYPE: Journal
LANGUAGE: English

AB From an **E. coli purine** auxotroph a mutant defective in **phosphoribosyl pyrophosphate synthetase** (I) was isolated and partially characterized. In contrast to the parental strain, the mutant was able to grow on **nucleosides** as **purine** source, whereas growth on **purine** bases was reduced. Kinetic anal. of the mutant I revealed an apparent Km for ATP and ribose 5-phosphate of 1.0 mM and 240 .mu.M, resp., compared to 60 and 45 .mu.M, resp., for the wild-type enzyme. ADP, which inhibits wild-type I at a concn. of 0.5 mM ribose 5-phosphate, stimulated mutant I. The activity of I in crude ext. was higher in the mutant than in the parent. When starved for **purines**, an accumulation of phosphoribosyl pyrophosphate was obsd. in the parent

strain, whereas the pool decreased in the mutant. During pyrimidine starvation derepression of I activity was obsd. in both strains, although to a lesser extent in the mutant. Presumably, the mutant harbors a mutation in the structural gene for I. The mutation responsible for the altered I was located in the purB-hemA region at 26 min on the recalibrated linkage map.